

Structure of HTPL and alignment of Patched motifs.

FIG. 1A

HTPL-L (954 a.a.)

HTPL-S (767 a.a.)



FIG. 1B

Patched motif

Patched motif		10	20	30	40	50	60	70	80
consensus	*********							
HTPL-L		1 VLSSKIRYTFTPDDIRSYTERGSRSEHEPL-VERKFFPGDGYPISRFSIIITAKARNS-NILDIRXLNEVVQVNDFFISTNV							
gi 1825729		162 deedeel eehyTPVGPSPAKAERRFVQGHFTTnDSYRFSASRRSTEANFVSLILVVSYS-D-SLLDPATFAEVSKLDGAVQDLR							
gi 1707052		47 NPLSDAVYLFTPLGAQSKMERMSIHEKWPL-TDNNYIPGRAVTSQREIQVTALARNDsNILDPKFANAVYQLDKYIQTRV							
gi 3892144		22 NVVYSLIMIFGPPY---SYTERRIIHDAWPL-VDGTFVAGRAVTSQREVQVAVVARSgGNILDRVFSNELKLMEsFTFNNI							
		49 LRVDPPSYVFTPSDARWRREISVFENWPL-DENKFLPGKSFEAKRFVNILIRAKDGgS IMRDNVLHHEIEILNQWIMNNI							
consensus	*********							
HTPL-L		79 TIPVSG--ITLSFKDLCMRFCDINCPVNOHYNGQILRSNLHNSRIDLTYPMTTFGTKIYLGPNFGGVKLDPN---							
gi 1825729		241 VAREKG--SQIQYQVCARYALCVPPNPILYAWQVKNKTILNS--SISPPAYNHGRHPLYLITGFFGGYILGGS---							
gi 1707052		126 RVLHNG--HYYSYKNILCLQYKNGGCPSNKHV---HILSDLNHGFNITYPYFRFGSEGGYIGSSLGGVTVMKgeneTDI-							
gi 3892144		98 TVQFSN--RTWSFADILCLAGpDGRcANNdHI---QLASRLHQHGINITYPTVRLSDKSAYIASALGGVVKLAKgdngeNI-							
		128 SIPTDDdlkFNLTyQDILCLSY-DWVCgANEHIQ-MLLRRNDVNQILDLHFPRGGTKDTPVYLGIGIFGDVQFFQn-----GT-							

FIG. 1B

Patched motif (Continued)

	170	180	190	200	210	220	230	240			
consensus	153	--IKSVKAI	VL	YRLKRD	PEEVED	SKEWEL	SFDYLE	NEYASD	-HIQ-VTIFSDQVLED--ELVRNGLTLTPFFVVGFA	226	
HTPL-L	314	qLLRAKAM	RLLYL	KTEDPE	YDVQSK	QWLTHL	LDQFTN	IKNIL-ALKKIE	VVHTSLSRqlEFEATSVTVIPVHFLAYI	392	
gi 1825729	200	--LASAKA	WFMIYH	LKFHEP	EMSISY	SGEWELE	GRMLTQ	YPEDP-YIS-ITYFHSQ	TAD--ELKRNADTLIPRFIISIT	273	
gi 1707052	172	--IVEATA	WLLIYQ	LKFPNE	ISYVSG	LWEREF	KNKMDY	KKQAKYIS-ITYFHSQ	TLD--ELNRNAERLAPKFIGAFV	246	
gi 3892144	201	--LSDAKL	TQLFYF	LKQDKQ	KWVEEY	SSKFSYA	LETFLN	QVYSSD-VIT-LSFAHYQ	SLED--GLDENAKAFVNFVVSFF	274	
	250	260	270	280	290	300	310	320			
consensus	227	ILVTFSIL	TSVRLAS	-GSLHID	WVRSKP	ILAILGV	LTPLM	AIIVSA	FGLLFWLGFRFNSIVCVMPLVL--	293	
HTPL-L	393	LIILFAV	TSCFRF	-----	DCIRNK	MCVAA	FGVISAF	LA	VSGFGLLHLHIGVPFVIIVANSPLIL--	452	
gi 1825729	274	LLIVFST	LCSLSF	ID-GSFS	IDWVLS	KPILSIL	GVVSAG	IAILTG	VGFLSIMGMPYNDIVGVMPFLVL--	340	
gi 1707052	247	ILVCFSV	LCSIVT	IK-GSGY	IDWVTK	PILSVL	GVSNAG	MIASAM	GLTYLEIQYNDIIA	274	
gi 3892144	275	VLAMYAL	VSSFTL	KSsATK	IDWISS	KPWLA	AGMFST	VLIIIS	AFGLFILGVRYNVINTIIPFLI	354	
	330	340	350	360	370	380	390	400			
consensus	294	--AIGVDD	MFLMVH	AQWRTT	RSLSV	KKRMGE	VLEEAG	PSITIT	SLTNVLSFGIGAITTPTPEIQ	370	
HTPL-L	453	---GVGV	DDMFIM	ISA	WHKTN	LAGDIR	ERMSNV	YSKAAV	SITITITN	ILALYTGIMSSFRSVQCFCIYGTTLFCYFY	529
gi 1825729	341	---AVG	VDNMFL	MVA	AVRRTS	RTHVHER	MGECL	ADA	AAVSILITSS	TDVLSFGVGAITTIPAVQIFCVYTGVAIFPAFIY	417
gi 1707052	314	---AVG	TDNMFL	MVAS	LKRTDR	NLKYDQ	RIAE	CMADA	AAVSILIT	ALTALD	390
gi 3892144	355	qiPAIG	IDDMFL	MNAC	WDQTS	KSLSV	PERMSK	TL	SHAGVAVTITNV	TDVMSFAIGCITDLP	434
	410	420	430	440	450	460	470	480			
consensus	371	QLTFFAA	IMAIAG	KYEMK	GRHSL	FLR---	AVDAAE	TESP---	QRLDSRGS	AK-----	416
HTPL-L	530	NITCFGA	FMALDG	KRE---	VVCLC	W---L	KKADP	KWPS---	FKKFC	CFPF	571
gi 1825729	418	QITFFAA	CLALAM	KEASGR	NLSFL	lie---	AVSAE	KKTS	Lst--fQRLFN	GLSV	468
gi 1707052	391	QLTFFCA	ILVYTR	IEEQGL	HSIWL	Rp---	AVTYS	STS	PLn---VKLFW	GLSQP	450
gi 3892144	435	QLTFFSG	AMAIMGE	VEREK	RHCLFF	Yrtf	qLVDI	SKMNEE	adsklQ	QIKRSAS	514

FIG. 1

FIG. 1B

Patched motif (Continued)

	490	500	510	520	530	540	550	560	
consensus	417	475	550	560	570	580	590	600	610
HTPL-L	572	632	640	650	660	670	680	690	700
gi 1825729	469	528	530	540	550	560	570	580	590
gi 1707052	451	522	530	540	550	560	570	580	590
gi 3892144	515	592	600	610	620	630	640	650	660
consensus	476	555	630	640	650	660	670	680	690
HTPL-L	633	709	710	720	730	740	750	760	770
gi 1825729	529	607	610	620	630	640	650	660	670
gi 1707052	523	600	610	620	630	640	650	660	670
gi 3892144	593	671	680	690	700	710	720	730	740
consensus	556	633	710	720	730	740	750	760	770
HTPL-L	710	779	780	790	800	810	820	830	840
gi 1825729	608	685	690	700	710	720	730	740	750
gi 1707052	601	676	680	690	700	710	720	730	740
gi 3892144	672	744	750	760	770	780	790	800	810
consensus	634	686	738	745	750	760	770	780	790
HTPL-L	780	832	840	850	860	870	880	890	900
gi 1825729	686	738	745	750	760	770	780	790	800
gi 1707052	677	729	738	745	750	760	770	780	790
gi 3892144	745	824	830	840	850	860	870	880	890

FIG. 1B

Patched motif (Continued)

		810	820	830	840	850	860	870	880	
consensus	**********								
HTPL-L	687	ASIDIGVFGFLSLWGVLDLPISMITI	IMSIGFSVD	FSAHIAHYF	YRSHGSETP	DERLADALEAL	GWPV	IQAALSTIL	CVL	766
gi 1825729	833	GSVIVGVTFGMAFWKVNLD	SISMINLV	ICTGFS	DFSAHISYAFV	-SSSQPSV	NQKSVEAL	YLLGYP	VLQSAIST	911
gi 1707052	739	ASIDFGVIGYMTLWGVNLD	DAISMITI	IMSIGFSVD	YSAHIAYG	VVVSRED	-TAAGR	VKEALSAL	GWPLSQ	817
gi 3892144	730	GSIDLGVLGFWMTLWNVNLD	DAISMITI	IMSVGFSVD	YSAHITYAY	VISKES	-TTSAR	VCDALG	DLGW	808
	825	VGINIGVFGYMTLWGVNLD	AVSMISI	IMSIGFAVD	LSAHIIYAFV	TSHG	-DTKQR	VIGALE	ETL	902
		890	900	910	920	930	940			
consensus	********								
HTPL-L	767	PLLFVPSYMWVFFKTI	FLVWVIG	LHGLIF	LPIILSL	FVT-----	IRTSNA	KIKKPSSI		821
gi 1825729	912	VLAATAKAYIFRTFF	KIMFLVM	IFGAHGL	IFIPVFL	TFFGRfi-----				954
gi 1707052	818	VLADIPAYMIVTFFK	TVVLSIS	LGLHGLV	FLPVL	LSIFVR	gccii	psphGHP	SAQKIE	882
gi 3892144	809	VLSDVPAYMIVTFFK	TVFLAIS	IGFLHGL	VFLPL	MLSVFV	Gki-----	fdIHIS	NI	867
	903	ILYTVDAYIILVFFK	TIWLTML	IGAIGHGL	FFIP	IFLSL	FPV-----	EFFRIP	KSSEL	954

Structure of the HTPL gene (Chr. 10p12.1)

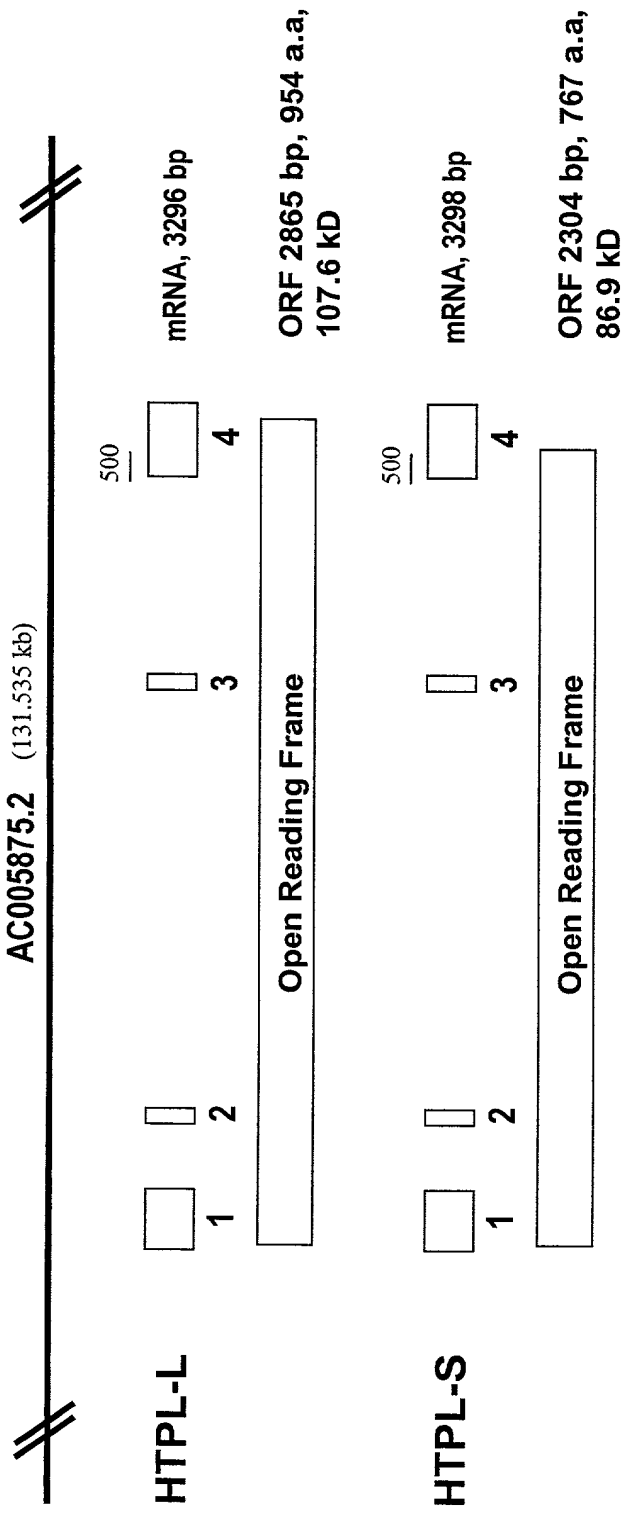


FIG. 2

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[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

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S	R	T	F	Q	W	L	G	W	Q	V	G	A	136
TCC	CGC	ACC	TTC	CAG	TGG	CTG	GGG	TGG	CAG	GTG	GGC	GCG	485
H	P	W	I	F	L	L	A	P	L	M	L	T	149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA	524
A	A	L	G	T	G	F	L	Y	L	P	K	D	162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC	563
E	E	E	D	L	E	E	H	Y	T	P	V	G	175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG	602
S	P	A	K	A	E	R	R	F	V	Q	G	H	188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTG	CAG	GGC	CAT	641
F	T	T	N	D	S	Y	R	F	S	A	S	R	201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG	680
R	S	T	E	A	N	F	V	S	L	L	V	V	214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC	719
S	Y	S	D	S	L	L	D	P	A	T	F	A	227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA	758
E	V	S	K	L	D	G	A	V	Q	D	L	R	240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC	797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q	253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG	836
V	C	A	R	Y	R	A	L	C	V	P	P	N	266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC	875
P	I	L	Y	A	W	Q	V	N	K	T	L	N	279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC	914
L	S	S	I	S	F	P	A	Y	N	H	G	R	292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG	953
H	P	L	Y	L	T	G	F	F	G	G	Y	I	305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC	992

FIG. 3

L	G	G	S	L	G	M	G	Q	L	L	L	R	318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG	1031
A	K	A	M	R	L	L	Y	Y	L	K	T	E	331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG	1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T	344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC	1109
H	L	L	D	Q	F	T	N	I	K	N	I	L	357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG	1148
A	L	K	K	I	E	V	V	H	F	T	S	L	370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT	1187
S	R	Q	L	E	F	E	A	T	S	V	T	V	383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG	1226
I	P	V	F	H	L	A	Y	I	L	I	I	L	396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG	1265
F	A	V	T	S	C	F	R	F	D	C	I	R	409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA	1304
N	K	M	C	V	A	A	F	G	V	I	S	A	422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT	1343
F	L	A	V	V	S	G	F	G	L	L	L	H	435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC	1382
I	G	V	P	F	V	I	I	V	A	N	S	P	448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA	1421
F	L	I	L	G	V	G	V	D	D	M	F	I	461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC	1460
M	I	S	A	W	H	K	T	N	L	A	G	D	474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GGT	GAC	1499
I	R	E	R	M	S	N	V	Y	S	K	A	A	487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA	1538

FIG. 3

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V	S	I	T	I	T	T	I	T	N	I	L	A	500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC	1577
L	Y	T	G	I	M	S	S	F	R	S	V	Q	513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCC	GTA	CAA	1616
C	F	C	I	Y	T	G	T	T	L	L	F	C	526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ACG	ACC	CTG	TTA	TTT	TGC	1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A	539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC	1694
L	D	G	K	R	E	V	V	C	L	C	W	L	552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG	1733
K	K	A	D	P	K	W	P	S	F	K	K	F	565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC	1772
C	C	F	P	F	G	S	V	P	D	E	H	G	578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA	1811
T	D	I	H	P	M	S	L	F	F	R	D	Y	591
ACT	GAT	ATC	CAT	CCA	ATG	AGT	TTG	TTT	TTT	AGA	GAC	TAT	1850
F	G	P	F	L	T	R	S	E	S	K	Y	F	604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT	1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I	617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA	1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R	630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA	1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F	643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT	2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R	656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG	2045
V	M	V	I	V	T	K	K	V	D	Y	W	D	669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT	2084

FIG. 3

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K	D	V	R	Q	K	L	E	N	C	T	K	I	682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT	2123
F	E	K	N	V	Y	V	D	K	N	L	T	E	695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG	2162
F	W	L	D	A	Y	V	Q	Y	L	K	G	N	708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
S	Q	D	P	N	E	K	N	T	F	M	N	N	721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
D	I	N	I	S	S	S	N	E	I	I	S	S	747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I	Q	T	T	D	V	S	S	S	A	760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
K	K	K	I	L	L	F	Q	L	R	R	I	A	773
AAA	AAG	AAA	ATA	TTG	TTA	TTC	CAA	TTA	CGA	CGC	ATA	GCT	2396
E	D	C	Q	I	P	L	M	V	Y	N	Q	A	786
GAA	GAC	TGT	CAA	ATT	CCC	CTA	ATG	GTG	TAT	AAC	CAG	GCA	2435
F	I	Y	F	D	Q	Y	A	A	I	L	E	D	799
TTT	ATA	TAT	TTT	GAT	CAG	TAT	GCT	GCA	ATA	TTA	GAA	GAC	2474
T	V	R	N	V	L	V	A	S	A	A	M	F	812
ACT	GTT	AGA	AAT	GTA	TTG	GTT	GCA	TCA	GCA	GCT	ATG	TTC	2513
I	V	S	L	L	L	I	P	Y	P	L	C	S	825
ATT	GTT	TCC	TTA	TTG	TTA	ATC	CCT	TAT	CCA	TTG	TGT	TCC	2552
L	W	V	T	F	A	I	G	S	V	I	V	G	838
TTG	TGG	GTG	ACT	TTT	GCT	ATC	GGT	TCT	GTG	ATT	GTA	GGG	2591
V	T	G	F	M	A	F	W	K	V	N	L	D	851
GTA	ACG	GGT	TTC	ATG	GCA	TTC	TGG	AAA	GTC	AAT	CTT	GAT	2630

FIG. 3

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S	I	S	M	I	N	L	V	I	C	T	G	F	864
TCC	ATA	TCC	ATG	ATT	AAT	CTT	GTC	ATT	TGT	ACA	GGG	TTT	2669
S	F	D	F	S	A	H	I	S	Y	A	F	V	877
TCT	TTC	GAT	TTT	TCT	GCA	CAC	ATT	TCC	TAT	GCA	TTT	GTT	2708
S	S	S	Q	P	S	V	N	Q	K	S	V	E	890
TCT	AGT	TCT	CAA	CCC	TCA	GTA	AAC	CAA	AAA	TCA	GTT	GAG	2747
A	L	Y	L	L	G	Y	P	V	L	Q	S	A	903
GCA	TTG	TAT	CTT	CTA	GGC	TAC	CCA	GTG	TTA	CAA	AGT	GCA	2786
I	S	T	I	I	G	V	C	V	L	A	A	A	916
ATT	TCA	ACA	ATA	ATA	GGG	GTG	TGT	GTT	TTA	GCT	GCA	GCG	2825
K	A	Y	I	F	R	T	F	F	K	I	M	F	929
AAA	GCA	TAC	ATC	TTT	AGA	ACA	TTT	TTT	AAG	ATT	ATG	TTT	2864
L	V	M	I	F	G	A	A	H	G	L	I	F	942
CTT	GTT	ATG	ATA	TTT	GGG	GCA	GCT	CAT	GGC	CTA	ATT	TTT	2903
I	P	V	F	L	T	F	F	G	R	F	I	*	955
ATT	CCA	GTA	TTC	TTA	ACC	TTT	TTT	GGA	AGG	TTT	ATT	TGA	2942
ATATCCACTAACAAGTCAAAGACCAATTCTAGAATTCCTGATTGCCCTATTC													2994
CAATCTGATTTTTTTTAAATGCACTATTAAGAATAGTCAACAAACTACTGGGA													3046
GGCCAAAGTGGGTGGATCACCTGAGGTCAAGAATTCGAGACCAGCCTGGCCA													3098
ACATGGTGAAACCTCGACACTACTGAAAATACAAAAATTATCCAGGCATGGT													3150
GGCGTGACCTATAATCCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCT													3202
TGAACCTGGGAGATGGAGGTTGCAGTGAGCTGGAGTGCACCAGGCACTCCAG													3254
CCTGGGTGACAAGAATGAGACTCCGTCTCAGAAAAAAAAAAAA													3296

FIG. 3

[illegible]

HTPL-S

nt: SEQ ID NO: 4

aa: SEQ ID NO: 6

CAGGAAACCGTCTGGTG	GATCTCCGCAGCTGCTTTTCACCTGCTGTTCCTC		52
	M P W V E P		6
CTGCGCTTCCTAAGAGGAAGAATCA	ATG CCG TGG GTG GAG CCC		95
K P R P G P E Q K P K L T			19
AAG CCC AGG CCG GGG CCG GAG CAG AAG CCC AAG CTC ACC			134
K P D S A T G P Q W Y Q E			32
AAA CCG GAC TCT GCC ACC GGG CCG CAG TGG TAC CAG GAA			173
S Q E S E S E G K Q P P P			45
TCT CAG GAA TCG GAG TCG GAA GGC AAG CAG CCA CCC CCG			212
G P L A P P K S P E P S G			58
GGA CCC CTG GCA CCC CCG AAA TCC CCC GAA CCC TCA GGA			251
P L A S E Q D A P L P E G			71
CCC CTG GCG TCG GAG CAG GAT GCA CCC CTG CCA GAG GGG			290
D D A P P R P S M L D D A			84
GAC GAT GCA CCC CCC CGG CCG TCG ATG CTG GAC GAT GCA			329
P R L P L E L D D A P L P			97
CCC CGC CTG CCG CTG GAG CTG GAC GAT GCA CCC CTG CCG			368
E E E T P E P T A I C R H			110
GAG GAG GAA ACC CCC GAA CCC ACG GCC ATC TGC AGG CAC			407
R H R C H T D C L E G L L			123
CGG CAC CGC TGT CAC ACC GAC TGC CTA GAG GGG CTG CTG			446
S R T F Q W L G W Q V G A			136
TCC CGC ACC TTC CAG TGG CTG GGG TGG CAG GTG GGC GCG			485

FIG. 4

H	P	W	I	F	L	L	A	P	L	M	L	T	149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA	524
A	A	L	G	T	G	F	L	Y	L	P	K	D	162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC	563
E	E	E	D	L	E	E	H	Y	T	P	V	G	175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG	602
S	P	A	K	A	E	R	R	F	V	Q	G	H	188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTG	CAG	GGC	CAT	641
F	T	T	N	D	S	Y	R	F	S	A	S	R	201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG	680
R	S	T	E	A	N	F	V	S	L	L	V	V	214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC	719
S	Y	S	D	S	L	L	D	P	A	T	F	A	227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA	758
E	V	S	K	L	D	G	A	V	Q	D	L	R	240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC	797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q	253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG	836
V	C	A	R	Y	R	A	L	C	V	P	P	N	266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC	875
P	I	L	Y	A	W	Q	V	N	K	T	L	N	279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC	914
L	S	S	I	S	F	P	A	Y	N	H	G	R	292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG	953
H	P	L	Y	L	T	G	F	F	G	G	Y	I	305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC	992
L	G	G	S	L	G	M	G	Q	L	L	L	R	318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG	1031

FIG. 4

A	K	A	M	R	L	L	Y	Y	L	K	T	E	331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG	1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T	344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC	1109
H	L	L	D	Q	F	T	N	I	K	N	I	L	357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG	1148
A	L	K	K	I	E	V	V	H	F	T	S	L	370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT	1187
S	R	Q	L	E	F	E	A	T	S	V	T	V	383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG	1226
I	P	V	F	H	L	A	Y	I	L	I	I	L	396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG	1265
F	A	V	T	S	C	F	R	F	D	C	I	R	409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA	1304
N	K	M	C	V	A	A	F	G	V	I	S	A	422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT	1343
F	L	A	V	V	S	G	F	G	L	L	L	H	435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC	1382
I	G	V	P	F	V	I	I	V	A	N	S	P	448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA	1421
F	L	I	L	G	V	G	V	D	D	M	F	I	461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC	1460
M	I	S	A	W	H	K	T	N	L	A	D	D	474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GAT	GAC	1499
I	R	E	R	M	S	N	V	Y	S	K	A	A	487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA	1538
V	S	I	T	I	T	T	I	T	N	I	L	A	500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC	1577

FIG. 4

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L	Y	T	G	I	M	S	S	F	R	S	V	Q	513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCT	GTA	CAA	1616
C	F	C	I	Y	T	G	M	T	L	L	F	C	526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ATG	ACC	CTG	TTA	TTT	TGC	1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A	539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC	1694
L	D	G	K	R	E	V	V	C	L	C	W	L	552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG	1733
K	K	A	D	P	K	W	P	S	F	K	K	F	565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC	1772
C	C	F	P	F	G	S	V	P	D	E	H	G	578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA	1811
T	D	I	H	P	I	S	L	F	F	R	D	Y	591
ACT	GAT	ATC	CAT	CCA	ATA	AGT	TTG	TTT	TTT	AGA	GAC	TAT	1850
F	G	P	F	L	T	R	S	E	S	K	Y	F	604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT	1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I	617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA	1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R	630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA	1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F	643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT	2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R	656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG	2045
V	M	V	I	V	T	K	K	V	D	Y	W	D	669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT	2084
K	D	V	R	Q	K	L	E	N	C	T	K	I	682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT	2123
F	E	K	N	V	Y	V	D	K	N	L	T	E	695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG	2162

FIG. 4

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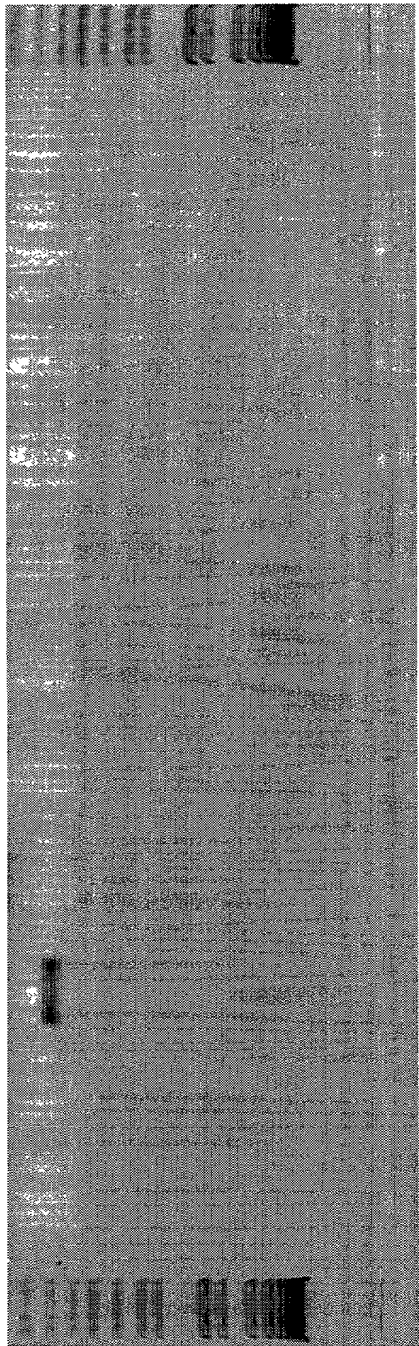
F	W	L	D	A	Y	V	Q	Y	L	K	G	N	708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
S	Q	D	P	N	E	K	N	T	F	M	N	N	721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
D	I	N	I	S	S	S	N	E	I	I	S	S	747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I	Q	T	T	D	V	S	S	S	A	760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
K	K	K	I	L	L	F	*						768
AAA	AAG	AAA	ATA	TTG	TTA	TTC	TAA	TTACGACGCATAGCTGAAG					2400
ACTGTCAAATTCCCCTAATGGTGTATAACCAGGCATTTATATATTTTGATCA													2452
GTATGCTGCAATATTAGAAGACACTGTTAGAAATGTATTGGTTGCATCAGCA													2504
GCTATGTTCAATTGTTTCCTTATTGTTAATCCCTTATCCATTGTGTTTCCTTGT													2556
GGGTGACTTTTGCTATTGGTTCTGTGATTGTAGGGGTAACGGGTTTCATGGC													2608
ATTCTGGAAAGTCAATCTTGATTCCATATCCATGATTAATCTTGTCATTTGT													2660
ATAGGGTTTTCTTTTCGATTTTTCTGTACACATTTTCCTATGCATTTGTTTCTA													2712
GTTCTCAACCCTCAGTAAACCAAAAATCAGTTGAGGCATTGTATCTTCTAGG													2764
CTACCCAGTGTTACAAAGTGCAATTTCAACAATAATAGGGGTGTGTGTTTTA													2816
GCTGCAGCGAAAGCATAACATCTTCAGAACATTTTTTAAGATTATGTTTCTTG													2868
TTATGATATTTGGGGCAGCTCATGGCCTAATTTTTATTCCAGTATTCTTAAC													2920
CTTTTTTGGAAGGTTTATTTGAATATCCACTAACAAGTCAAAGACCAATTCT													2972
AGAATTCCTGATTGCCCTATTCCAATCTGATTTTTTTAAATGCACTATTAAG													3024
AATAGTCAACAACTACTGGGAGGCCAAGGTGGGTGGATCACCTGAGGTCAA													3076

FIG. 4

GAATTCGAGACCAGCCTGGCCAACATGGTGAAACCTCGACACTACTGAAAAT 3128
ACAAAAATTATCCAGGCATGGTGGCGTGACCTATAATCCCAGCTACCTGGG 3180
AGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGATGGAGGTTGCAGTGAGC 3232
TGGAGTGCACCAGGCACTCCAGCCTGGGTGACAAGAATGAGACTCCGTCTCA 3284
GAAAAAAAAAAAAA 3298

FIG. 4

HTPL →



HTPL tissue distribution by RT-PCR

FIG. 5